Sequence Listing

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<110> Chen, Jian
Filvaroff, Ellen
Goddard, Audrey
Gurney, Austin
Li, Hanzhong
Wood, William I.

<120> IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

<130> P1381-R1

<141> 1999-05-14

<150> US 60/085,579
<151> 1998-05-15

<150> US 60/113,621
<151> 1998-12-23

<160> 26

<210> 1
<211> 180
<212> PRT
<213> Homo sapiens

<400> 1

Met	Asp	Trp	Pro	His	Asn	Leu	Leu	Phe	Leu	Leu	Thr	Ile	Ser	Ile
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Phe	Leu	Gly	Leu	Gly	Gln	Pro	Arg	Ser	Pro	Lys	Ser	Lys	Arg	Lys
				20				25						30
Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val
				35				40						45
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu
				50				55						60
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn
				65				70						75
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu
				80				85						90

Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
95 100 105

Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
110 115 120

Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
125 130 135

Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
140 145 150

Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
155 160 165

Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
170 175 180

<210> 2
<211> 687
<212> DNA
<213> Homo sapiens

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cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100

ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150

ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200

aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250

ggcccagctg aggaacagct cagagctggc ccagagaaag tgtgaggtca 300

acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350

agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400

gtgcctgtgt ctgggctgtg tgaacccctt caccatgcag gaggaccgca 450

gcatggtgag cgtgccggtg ttcagccagg ttcctgtgcg ccgccgcctc 500

tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550

gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600

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ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 3
<211> 197
<212> PRT
<213> Homo sapiens

<400> 3

Met Thr Leu Leu Pro Gly Leu Leu Phe Leu Thr Trp Leu His Thr
1 5 10 15

Cys Leu Ala His His Asp Pro Ser Leu Arg Gly His Pro His Ser
20 25 30

His Gly Thr Pro His Cys Tyr Ser Ala Glu Glu Leu Pro Leu Gly
35 40 45

Gln Ala Pro Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln
50 55 60

Ala Leu Pro Val Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His
65 70 75

Arg Gly Arg His Glu Arg Pro Ser Ala Thr Thr Gln Cys Pro Val
80 85 90

Leu Arg Pro Glu Glu Val Leu Glu Ala Asp Thr His Gln Arg Ser
95 100 105

Ile Ser Pro Trp Arg Tyr Arg Val Asp Thr Asp Glu Asp Arg Tyr
110 115 120

Pro Gln Lys Leu Ala Phe Ala Glu Cys Leu Cys Arg Gly Cys Ile
125 130 135

Asp Ala Arg Thr Gly Arg Glu Thr Ala Ala Leu Asn Ser Val Arg
140 145 150

Leu Leu Gln Ser Leu Leu Val Leu Arg Arg Arg Pro Cys Ser Arg
155 160 165

Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe Ala Phe His Thr
170 175 180

Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val Leu Pro Arg
185 190 195

Ser Val
197

<210> 4
<211> 1047
<212> DNA
<213> Homo sapiens

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gcccaccatg acccctccct caggggcac ccccacagtc acggtacccc 150

acactgctac tcggctgagg aactgccccct cggccaggcc cccccacacc 200

tgctggctcg aggtgccaag tgggggcagg ctttgcctgt agccctggtg 250

tccagcctgg aggcagcaag ccacaggggg aggcacgaga ggccctcagc 300

tacgacccag tgcccggtgc tgcggccgga ggaggtgttg gaggcagaca 350

cccaccagcg ctccatctca ccctggagat accgtgtgga cacggatgag 400

gaccgctatc cacagaagct ggccttcgcc gagtgcctgt gcagaggctg 450

tatcgatgca cggacgggcc gcgagacagc tgcgctcaac tccgtgcggc 500

tgctccagag cctgctggtg ctgcgccgcc ggccctgctc ccgcgacggc 550

tcggggctcc ccacacctgg ggcctttgcc ttccacaccg agttcatcca 600

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cctgtcctgc tcccggcttc ccttacccta tcactggcct caggccccgc 950

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tatttaagtg tacgtgtatt attaaactga tgaacacatc cccaaaa 1047

<210> 5
<211> 830
<212> DNA
<213> Homo sapiens

<220>
<221> unknown
<222> 105-115
<223> unknown base

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cctggttctt gctccttggg actctgggac ttacaccagt ggcacccctg 100

gctcnnnnnn nnnnnaattc ggtacgaggc tggggttcag gcgggcagca 150

gctgcaggct gaccttgcag cttggcggaa tggactggcc tcacaacctg 200

ctgtttcttc ttaccatttc catcttcctg gggctgggcc agcccaggag 250

ccccaaaagc aagaggaagg ggcaagggcg gcctgggccc ctggtccctg 300

gccctcacca ggtgccactg gacctggtgt cacggatgaa accgtatgcc 350

cgcatggagg agtatgagag gaacatcgag gagatgttgg cccagctgag 400

gaacagttca gagctggccc agagaaagtg tgaggtcaac ttgcagctgt 450

ggatgtccaa caagaggagc ctgtctccct ggggctacag catcaaccac 500

gaccccagcc gtatccccgt ggacctccgg aggcacggtg cctgtgtctg 550

ggcttgtgtg aacccccttca ccatgcagga ggaccgcagc atggtgagcg 600

tgccggtgtt cagccaggtt cctgtgcgcc gccgcctctg cccgccaccg 650

ccccgcacag ggccttgccg ccagcgcgca gtcatggaga ccatcgctgt 700

gggctgcacc tgcatcttct gaatcgacct ggcccagaag ccaggccagc 750

agcccgagac catcctcctt gcacctttgt gccaagaaag gcctatgaaa 800

agtaaacact gacttttgaa agcaaaaaaa 830

<210> 6
<211> 397
<212> DNA
<213> Artificial

<220>
<221> unknown
<222> 10, 150, 267
<223> unknown base

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ctcacaacct gctgtttctt cttaccattt ccatcttcct ggggctgggc 100

agccaggagc cccaaaagca agaggaaggg gcaagggcgg cctgggcccn 150

tggcctggcc tcaccaggtg ccactggacc tggtgtcacg gatgaaaccg 200

tatgcccgca tggaggagta tgagaggaac atcgaggaga tggtggccca 250

gctgaggaac agctcanaag ctggcccaga gaaagtgtga ggtcaacttg 300

cagctgtgga tgtccaacaa gaaggagcct gtctcccttg gggctacaag 350

catcaaccac cgaccccagc cgtatccccg tgggaccttg ccgggac 397

<210> 7
<211> 230
<212> DNA
<213> Artificial

<400> 7
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gcagaggctg tatcgatgca cggacgggcc gcgagacagc tgcgctcaac 100

tccgtgcggc tgctccagag cctgctggtg ctgcgccgcc ggccctgctc 150

ccgcgacggc tcggggctcc ccacacctgg ggcctttgcc ttccacaccg 200

agttcatcca cgtccccgtc ggctgcacct 230

<210> 8
<211> 24

<212> DNA
<213> Artificial sequence

<400> 8
atccacagaa gctggccttc gccg 24

<210> 9
<211> 24
<212> DNA
<213> Artificial sequence

<400> 9
gggacgtgga tgaactcggt gtgg 24

<210> 10
<211> 40
<212> DNA
<213> Artificial sequence

<400> 10
tatccacaga agctggcctt cgccgagtgc ctgtgcagag 40

<210> 11
<211> 155
<212> PRT
<213> Human

<400> 11

Met	Thr	Pro	Gly	Lys	Thr	Ser	Leu	Val	Ser	Leu	Leu	Leu	Leu	Leu	
1				5				10						15	
Ser	Leu	Glu	Ala	Ile	Val	Lys	Ala	Gly	Ile	Thr	Ile	Pro	Arg	Asn	
				20				25						30	
Pro	Gly	Cys	Pro	Asn	Ser	Glu	Asp	Lys	Asn	Phe	Pro	Arg	Thr	Val	
				35				40						45	
Met	Val	Asn	Leu	Asn	Ile	His	Asn	Arg	Asn	Thr	Asn	Thr	Asn	Pro	
				50				55						60	
Lys	Arg	Ser	Ser	Asp	Tyr	Tyr	Asn	Arg	Ser	Thr	Ser	Pro	Trp	Asn	
				65				70						75	
Leu	His	Arg	Asn	Glu	Asp	Pro	Glu	Arg	Tyr	Pro	Ser	Val	Ile	Trp	
				80				85						90	
Glu	Ala	Lys	Cys	Arg	His	Leu	Gly	Cys	Ile	Asn	Ala	Asp	Gly	Asn	
				95				100						105	

Val Asp Tyr His Met Asn Ser Val Pro Ile Gln Gln Glu Ile Leu
110 115 120

Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser Phe Arg Leu
125 130 135

Glu Lys Ile Leu Val Ser Val Gly Cys Thr Cys Val Thr Pro Ile
140 145 150

Val His His Val Ala
155

<210> 12
<211> 408
<212> PRT
<213> Artificial

<220>
<223> Artificial Sequence 1-408

<400> 12
Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
1 5 10 15

Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
20 25 30

Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
35 40 45

Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
50 55 60

Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
65 70 75

Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
80 85 90

Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
95 100 105

Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
110 115 120

Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
125 130 135

```
Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
                140                 145                 150

Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
                155                 160                 165

Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
                170                 175                 180

Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
                185                 190                 195

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                200                 205                 210

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
                215                 220                 225

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
                230                 235                 240

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                245                 250                 255

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                260                 265                 270

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
                275                 280                 285

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
                290                 295                 300

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
                305                 310                 315

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
                320                 325                 330

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
                335                 340                 345

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
                350                 355                 360

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                365                 370                 375
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Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
380 385 390

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
395 400 405

Pro Gly Lys
408

<210> 13
<211> 425
<212> PRT
<213> Artificial

<220>
<223> Artificial Sequence 1-425

<400> 13
Met Thr Leu Leu Pro Gly Leu Leu Phe Leu Thr Trp Leu His Thr
1 5 10 15

Cys Leu Ala His His Asp Pro Ser Leu Arg Gly His Pro His Ser
20 25 30

His Gly Thr Pro His Cys Tyr Ser Ala Glu Glu Leu Pro Leu Gly
35 40 45

Gln Ala Pro Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln
50 55 60

Ala Leu Pro Val Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His
65 70 75

Arg Gly Arg His Glu Arg Pro Ser Ala Thr Thr Gln Cys Pro Val
80 85 90

Leu Arg Pro Glu Glu Val Leu Glu Ala Asp Thr His Gln Arg Ser
95 100 105

Ile Ser Pro Trp Arg Tyr Arg Val Asp Thr Asp Glu Asp Arg Tyr
110 115 120

Pro Gln Lys Leu Ala Phe Ala Glu Cys Leu Cys Arg Gly Cys Ile
125 130 135

Asp Ala Arg Thr Gly Arg Glu Thr Ala Ala Leu Asn Ser Val Arg
140 145 150

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Leu Leu Gln Ser Leu Leu Val Leu Arg Arg Arg Pro Cys Ser Arg
                155                 160                 165

Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe Ala Phe His Thr
            170                 175                 180

Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val Leu Pro Arg
        185                 190                 195

Ser Val Pro Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
    200                 205                 210

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
215                 220                 225

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
            230                 235                 240

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
        245                 250                 255

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
    260                 265                 270

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
275                 280                 285

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
            290                 295                 300

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
        305                 310                 315

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
    320                 325                 330

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
335                 340                 345

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
            350                 355                 360

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
        365                 370                 375

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
    380                 385                 390
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Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
395 400 405

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
410 415 420

Leu Ser Pro Gly Lys
425

<210> 14
<211> 212
<212> PRT
<213> Homo sapiens

<400> 14
Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser
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Leu Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val
20 25 30

Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln
35 40 45

Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile
50 55 60

Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser
65 70 75

Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu
80 85 90

Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly
95 100 105

Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu
110 115 120

Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser
125 130 135

Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu
140 145 150

Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr
155 160 165

Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln
170 175 180

Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu
185 190 195

Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg
200 205 210

Gln Met
212

<210> 15
<211> 320
<212> PRT
<213> Homo sapiens

<400> 15
Met Gly Ala Ala Arg Ser Pro Pro Ser Ala Val Pro Gly Pro Leu
1 5 10 15

Leu Gly Leu Leu Leu Leu Leu Leu Gly Val Leu Ala Pro Gly Gly
20 25 30

Ala Ser Leu Arg Leu Leu Asp His Arg Ala Leu Val Cys Ser Gln
35 40 45

Pro Gly Leu Asn Cys Thr Val Lys Asn Ser Thr Cys Leu Asp Asp
50 55 60

Ser Trp Ile His Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp
65 70 75

Leu Gln Ile Gln Leu His Phe Ala His Thr Gln Gln Gly Asp Leu
80 85 90

Phe Pro Val Ala His Ile Glu Trp Thr Leu Gln Thr Asp Ala Ser
95 100 105

Ile Leu Tyr Leu Glu Gly Ala Glu Leu Ser Val Leu Gln Leu Asn
110 115 120

Thr Asn Glu Arg Leu Cys Val Arg Phe Glu Phe Leu Ser Lys Leu
125 130 135

Arg His His His Arg Arg Trp Arg Phe Thr Phe Ser His Phe Val
140 145 150

Val Asp Pro Asp Gln Glu Tyr Glu Val Thr Val His His Leu Pro
155 160 165

Lys Pro Ile Pro Asp Gly Asp Pro Asn His Gln Ser Lys Asn Phe
170 175 180

Leu Val Pro Asp Cys Glu His Ala Arg Met Lys Val Thr Thr Pro
185 190 195

Cys Met Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr Val Glu
200 205 210

Thr Leu Glu Ala His Gln Leu Arg Val Ser Phe Thr Leu Trp Asn
215 220 225

Glu Ser Thr His Tyr Gln Ile Leu Leu Thr Ser Phe Pro His Met
230 235 240

Glu Asn His Ser Cys Phe Glu His Met His His Ile Pro Ala Pro
245 250 255

Arg Pro Glu Glu Phe His Gln Arg Ser Asn Val Thr Leu Thr Leu
260 265 270

Arg Asn Leu Lys Gly Cys Cys Arg His Gln Val Gln Ile Gln Pro
275 280 285

Phe Phe Ser Ser Cys Leu Asn Asp Cys Leu Arg His Ser Ala Thr
290 295 300

Val Ser Cys Pro Glu Met Pro Asp Thr Pro Glu Pro Ile Pro Asp
305 310 315

Tyr Met Pro Leu Trp
320

<210> 16
<211> 543
<212> DNA
<213> Homo sapiens

<400> 16
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ggcctgggcc cctggcccct ggccctcacc aggtgccact ggacctggtg 150

tcacggatga aaccgtatgc ccgcatggag gagtatgaga ggaacatcga 200

ggagatggtg gcccagctga ggaacagctc agagctggcc cagagaaagt 250

gtgaggtcaa cttgcagctg tggatgtcca acaagaggag cctgtctccc 300

tggggctaca gcatcaacca cgaccccagc cgtatccccg tggacctgcc 350

ggaggcacgg tgcctgtgtc tgggctgtgt gaacccccttc accatgcagg 400

aggaccgcag catggtgagc gtgccggtgt tcagccaggt tcctgtgcgc 450

cgccgcctct gcccgccacc gccccgcaca gggccttgcc gccagcgcgc 500

agtcatggag accatcgctg tgggctgcac ctgcatcttc tga 543

<210> 17
<211> 594
<212> DNA
<213> Homo sapiens

<400> 17
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ggcccaccat gacccctccc tcaggggca cccccacagt cacggtaccc 100

cacactgcta ctcggctgag gaactgcccc tcggccaggc ccccccacac 150

ctgctggctc gaggtgccaa gtgggggcag gctttgcctg tagccctggt 200

gtccagcctg gaggcagcaa gccacagggg gaggcacgag aggccctcag 250

ctacgaccca gtgcccggtg ctgcggccgg aggaggtgtt ggaggcagac 300

acccaccagc gctccatctc accctggaga taccgtgtgg acacggatga 350

ggaccgctat ccacagaagc tggccttcgc cgagtgcctg tgcagaggct 400

gtatcgatgc acggacgggc cgcgagacag ctgcgctcaa ctccgtgcgg 450

ctgctccaga gcctgctggt gctgcgccgc cggccctgct cccgcgacgg 500

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acgtccccgt cggctgcacc tgcgtgctgc cccgttcagt gtga 594

<210> 18

<211> 9
<212> PRT
<213> Artificial

<220>
<223> Artificial sequence 1-9

<400> 18
Gly His His His His His His His His
1 5 9

<210> 19
<211> 157
<212> PRT
<213> Homo sapiens

<400> 19
Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
1 5 10 15

Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn
20 25 30

Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp
35 40 45

Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser
50 55 60

Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu
65 70 75

Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys
80 85 90

Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
95 100 105

Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
110 115 120

Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu
125 130 135

Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val
140 145 150

Tyr Phe Gly Ile Ile Ala Leu

155 157

<210> 20
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Artificial sequence 1-21

<400> 20
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<210> 21
<211> 58
<212> DNA
<213> Artificial

<220>
<223> Artificial sequence 1-58

<400> 21
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tgtagtcc 58

<210> 22
<211> 328
<212> PRT
<213> Homo sapiens

<400> 22

Met	Gly	Ala	Ala	Arg	Ser	Pro	Pro	Ser	Ala	Val	Pro	Gly	Pro	Leu	
1				5				10						15	
Leu	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Val	Leu	Ala	Pro	Gly	Gly	
				20				25						30	
Ala	Ser	Leu	Arg	Leu	Leu	Asp	His	Arg	Ala	Leu	Val	Cys	Ser	Gln	
				35				40						45	
Pro	Gly	Leu	Asn	Cys	Thr	Val	Lys	Asn	Ser	Thr	Cys	Leu	Asp	Asp	
				50				55						60	
Ser	Trp	Ile	His	Pro	Arg	Asn	Leu	Thr	Pro	Ser	Ser	Pro	Lys	Asp	
				65				70						75	

```
Leu Gln Ile Gln Leu His Phe Ala His Thr Gln Gln Gly Asp Leu
                80                  85                  90

Phe Pro Val Ala His Ile Glu Trp Thr Leu Gln Thr Asp Ala Ser
                95                 100                 105

Ile Leu Tyr Leu Glu Gly Ala Glu Leu Ser Val Leu Gln Leu Asn
               110                 115                 120

Thr Asn Glu Arg Leu Cys Val Arg Phe Glu Phe Leu Ser Lys Leu
               125                 130                 135

Arg His His His Arg Arg Trp Arg Phe Thr Phe Ser His Phe Val
               140                 145                 150

Val Asp Pro Asp Gln Glu Tyr Glu Val Thr Val His His Leu Pro
               155                 160                 165

Lys Pro Ile Pro Asp Gly Asp Pro Asn His Gln Ser Lys Asn Phe
               170                 175                 180

Leu Val Pro Asp Cys Glu His Ala Arg Met Lys Val Thr Thr Pro
               185                 190                 195

Cys Met Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr Val Glu
               200                 205                 210

Thr Leu Glu Ala His Gln Leu Arg Val Ser Phe Thr Leu Trp Asn
               215                 220                 225

Glu Ser Thr His Tyr Gln Ile Leu Leu Thr Ser Phe Pro His Met
               230                 235                 240

Glu Asn His Ser Cys Phe Glu His Met His His Ile Pro Ala Pro
               245                 250                 255

Arg Pro Glu Glu Phe His Gln Arg Ser Asn Val Thr Leu Thr Leu
               260                 265                 270

Arg Asn Leu Lys Gly Cys Cys Arg His Gln Val Gln Ile Gln Pro
               275                 280                 285

Phe Phe Ser Ser Cys Leu Asn Asp Cys Leu Arg His Ser Ala Thr
               290                 295                 300

Val Ser Cys Pro Glu Met Pro Asp Thr Pro Glu Pro Ile Pro Asp
               305                 310                 315
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Tyr Met Pro Leu Trp His His His His His His His His
320 325 328

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<400> 23
Ile Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg
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Lys Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln
20 25 30

Val Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met
35 40 45

Glu Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg
50 55 60

Asn Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln
65 70 75

Leu Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser
80 85 90

Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala
95 100 105

Arg Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu
110 115 120

Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val
125 130 135

Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg
140 145 150

Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile
155 160 165

Phe Gly His His His His His His His His
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<400> 24

Met Thr Leu Leu Pro Gly Leu Leu Phe Leu Thr Trp Leu His Thr
1 5 10 15

Cys Leu Ala His His Asp Pro Ser Leu Arg Gly His Pro His Ser
20 25 30

His Gly Thr Pro His Cys Tyr Ser Ala Glu Glu Leu Pro Leu Gly
35 40 45

Gln Ala Pro Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln
50 55 60

Ala Leu Pro Val Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His
65 70 75

Arg Gly Arg His Glu Arg Pro Ser Ala Thr Thr Gln Cys Pro Val
80 85 90

Leu Arg Pro Glu Glu Val Leu Glu Ala Asp Thr His Gln Arg Ser
95 100 105

Ile Ser Pro Trp Arg Tyr Arg Val Asp Thr Asp Glu Asp Arg Tyr
110 115 120

Pro Gln Lys Leu Ala Phe Ala Glu Cys Leu Cys Arg Gly Cys Ile
125 130 135

Asp Ala Arg Thr Gly Arg Glu Thr Ala Ala Leu Asn Ser Val Arg
140 145 150

Leu Leu Gln Ser Leu Leu Val Leu Arg Arg Arg Pro Cys Ser Arg
155 160 165

Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe Ala Phe His Thr
170 175 180

Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val Leu Pro Arg
185 190 195

Ser Val Gly His His His His His His His His
200 205 206

<210> 25
<211> 271
<212> PRT
<213> Homo sapiens

<400> 25

Met	Ala	Lys	Val	Pro	Asp	Met	Phe	Glu	Asp	Leu	Lys	Asn	Cys	Tyr		
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Ser	Glu	Asn	Glu	Glu	Asp	Ser	Ser	Ser	Ile	Asp	His	Leu	Ser	Leu		
				20					25						30	
Asn	Gln	Lys	Ser	Phe	Tyr	His	Val	Ser	Tyr	Gly	Pro	Leu	His	Glu		
				35					40						45	
Gly	Cys	Met	Asp	Gln	Ser	Val	Ser	Leu	Ser	Ile	Ser	Glu	Thr	Ser		
				50					55						60	
Lys	Thr	Ser	Lys	Leu	Thr	Phe	Lys	Glu	Ser	Met	Val	Val	Val	Ala		
				65					70						75	
Thr	Asn	Gly	Lys	Val	Leu	Lys	Lys	Arg	Arg	Leu	Ser	Leu	Ser	Gln		
				80					85						90	
Ser	Ile	Thr	Asp	Asp	Asp	Leu	Glu	Ala	Ile	Ala	Asn	Asp	Ser	Glu		
				95					100						105	
Glu	Glu	Ile	Ile	Lys	Pro	Arg	Ser	Ala	Pro	Phe	Ser	Phe	Leu	Ser		
				110					115						120	
Asn	Val	Lys	Tyr	Asn	Phe	Met	Arg	Ile	Ile	Lys	Tyr	Glu	Phe	Ile		
				125					130						135	
Leu	Asn	Asp	Ala	Leu	Asn	Gln	Ser	Ile	Ile	Arg	Ala	Asn	Asp	Gln		
				140					145						150	
Tyr	Leu	Thr	Ala	Ala	Ala	Leu	His	Asn	Leu	Asp	Glu	Ala	Val	Lys		
				155					160						165	
Phe	Asp	Met	Gly	Ala	Tyr	Lys	Ser	Ser	Lys	Asp	Asp	Ala	Lys	Ile		
				170					175						180	
Thr	Val	Ile	Leu	Arg	Ile	Ser	Lys	Thr	Gln	Leu	Tyr	Val	Thr	Ala		
				185					190						195	

Gln Asp Glu Asp Gln Pro Val Leu Leu Lys Glu Met Pro Glu Ile
200 205 210

Pro Lys Thr Ile Thr Gly Ser Glu Thr Asn Leu Leu Phe Phe Trp
215 220 225

Glu Thr His Gly Thr Lys Asn Tyr Phe Thr Ser Val Ala His Pro
230 235 240

Asn Leu Phe Ile Ala Thr Lys Gln Asp Tyr Trp Val Cys Leu Ala
245 250 255

Gly Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Asn Gln
260 265 270

Ala
271

<210> 26
<211> 177
<212> PRT
<213> Homo sapiens

<400> 26
Met Glu Ile Cys Arg Gly Leu Arg Ser His Leu Ile Thr Leu Leu
1 5 10 15

Leu Phe Leu Phe His Ser Glu Thr Ile Cys Arg Pro Ser Gly Arg
20 25 30

Lys Ser Ser Lys Met Gln Ala Phe Arg Ile Trp Asp Val Asn Gln
35 40 45

Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu
50 55 60

Gln Gly Pro Asn Val Asn Leu Glu Glu Lys Ile Asp Val Val Pro
65 70 75

Ile Glu Pro His Ala Leu Phe Leu Gly Ile His Gly Gly Lys Met
80 85 90

Cys Leu Ser Cys Val Lys Ser Gly Asp Glu Thr Arg Leu Gln Leu
95 100 105

Glu Ala Val Asn Ile Thr Asp Leu Ser Glu Asn Arg Lys Gln Asp
110 115 120

Lys	Arg	Phe	Ala	Phe	Ile	Arg	Ser	Asp	Ser	Gly	Pro	Thr	Thr	Ser
				125					130					135
Phe	Glu	Ser	Ala	Ala	Cys	Pro	Gly	Trp	Phe	Leu	Cys	Thr	Ala	Met
				140					145					150
Glu	Ala	Asp	Gln	Pro	Val	Ser	Leu	Thr	Asn	Met	Pro	Asp	Glu	Gly
				155					160					165
Val	Met	Val	Thr	Leu	Phe	Tyr	Phe	Gln	Glu	Asp	Glu			
				170					175		177			